What is Claimed is:

1. A process for the production of an L-amino acid product by fermentation comprising:
   a) culturing a recombinant microorganism from the Enterobacteriaceae family in a fermentation medium, wherein said recombinant microorganism produces said L-amino acid and wherein the yfiD ORF and/or the pflB gene are overexpressed in said recombinant microorganism or another nucleotide sequence that codes for the yfiD ORF product and/or the pflB gene product is expressed in said recombinant microorganism;
   b) enriching said L-amino acid in said fermentation medium or in said recombinant microorganism; and
   c) isolating said L-amino acid to produce said L-amino acid product.

2. The process of claim 1 wherein some or all of the constituents of said fermentation medium and/or the biomass of said recombinant microorganism remain in said L-amino acid product.

3. The process of claim 1, wherein said recombinant microorganism is made by the transformation of a microorganism of the Enterobacteriaceae family with a vector containing the yfiD ORF and/or the plfB gene.

4. The process of claim 1, wherein the number of copies of said pflB gene and/or said yfiD ORF in said recombinant microorganism is increased by at least 1.

5. The process of claim 4, wherein the increase in the number of copies of the yfiD ORF and/or of the pflB gene by at least 1 is achieved by integration of said gene or ORF into the chromosome of said recombinant microorganism.

6. The process of claim 4, wherein the increase in the number of copies of the yfiD ORF and/or of the pflB gene by at least 1 is achieved by means of an extra-chromosomally replicating vector.

7. The process of claim 1, wherein said overexpression is achieved by:
   a) mutating the promoter or the ribosome binding site upstream of said yfiD ORF and/or said pflB gene; or
   b) incorporating an expression cassette or promoter upstream of said yfiD ORF and/or of said pflB gene.

8. The process of claim 1, wherein said recombinant microorganism is made by the transformation of a microorganism with a polynucleotide coding for the yfiD ORF product and/or a pflB gene product and wherein the expression of said yfiD ORF product and/or a pflB gene product is under the control of a promoter.

9. The process of claim 1, wherein, through the recombinant engineering of the yfiD ORF and/or pflB gene, the concentration or activity of the YfiD gene product and/or of the PflB gene product (protein) is increased by at least 10 %, relative to the activity or concentration of the gene product in the initial strain.

10. The process of claim 1, wherein the genus of said recombinant microorganism is selected from the group consisting of: Escherichia; Erwinia; Providencia; and Serratia.

11. The process of claim 1, wherein, said microorganism overexpresses said yfiD ORF and/or said pflB gene, and, in addition, at least one gene in the biosynthesis pathway of said L-amino acid is also overexpressed.

12. The process of claim 1, wherein said microorganism overexpressed said yfiD ORF and/or said pflB gene, and, in addition, the activity of one or more additional genes is enhanced, said one or more additional genes being selected from the group consisting of:
   a) the thrABC operon coding for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase;
   b) the pyc gene coding for pyruvate carboxylase;
   c) the pps gene for phosphoenolpyruvate synthase;

d) the ppc gene coding for phosphoenolpyruvate carboxylase;

e) the genes pntA and pntB coding for transhydrogenase;

f) the rhtB gene imparting homoserine resistance;

g) the mqo gene coding for malate:quinone oxidoreductase;

h) the rhtC gene imparting threonine resistance;

i) the thrE gene coding for the threonine-export protein;

j) the gdhA gene coding for glutamate dehydrogenase;

k) the hns gene coding for the DNA binding protein HLP-II;

l) the pgm gene coding for phosphoglucomutase;

m) the fba gene coding for fructose biphosphate aldolase;

n) the ptsH gene coding for phosphohistidine protein hexose phosphotransferase;

o) the ptsI gene coding for enzyme I of the phosphotransferase system;

p) the crr gene coding for the glucose-specific IIA component;

q) the ptsG gene coding for the glucose-specific IIBC component;

r) the lrp gene coding for the regulator of the leucine regulon;

s) the csrA gene coding for the global regulator Csr;

t) the fadR gene coding for the regulator of the fad regulon;

u) the iclR gene coding for the regulator of central intermediary metabolism;

v) the mopB gene coding for the 10 kDa chaperon;

w) the ahpC gene coding for the small subunit of alkyl hydroperoxide reductase;

x) the ahpF gene coding for the large subunit of alkyl hydroperoxide reductase;

y) the cysK gene coding for cysteine synthase A;

z) the cysB gene coding for the regulator of the cys regulon;

aa) the cysJ gene coding for the flavoprotein of NADPH sulfite reductase;

bb) the cysI gene coding for the haemoprotein of NADPH sulfite reductase;

cc) the cysH gene coding for adenylyl sulfate reductase;

dd) the phoB gene coding for the positive regulator PhoB of the pho regulon;

ee) the phoR gene coding for the sensor protein of the pho regulon;

ff) the phoE gene coding for protein E of the outer cell membrane;

gg) the pykF gene coding for pyruvate kinase I, which is stimulated by fructose;

hh) the pfkB gene coding for 6-phosphofructokinase II;

ii) the malE gene coding for the periplasmic binding protein of maltose transport;

jj) the sodA gene coding for superoxide dismutase;

kk) the rseA gene coding for a membrane protein with anti-sigmaE activity;

ll) the rseC gene coding for a global regulator of the sigmaE factor;

mm) the sucA gene coding for the decarboxylase subunit of 2-ketoglutarate dehydrogenase;

nn) the sucB gene coding for the dihydrolipoyl transsuccinase E2 subunit of 2-ketoglutarate dehydrogenase;

oo) the sucC gene coding for the β-subunit of succinyl-CoA synthetase;

pp) the sucD gene coding for the α-subunit of succinyl-CoA synthetase;

qq) the adk gene coding for adenylate kinase;

rr) the hdeA gene coding for a periplasmic protein with chaperonin-type function;

ss) the hdeB gene coding for a periplasmic protein with chaperonin-type function;

tt) the icd gene coding for isocitrate dehydrogenase;

uu) the mglB gene coding for the periplasmic, galactose-binding transport protein;

vv) the lpd gene coding for dihydrolipoamide dehydrogenase;

ww) the aceE gene coding for the E1 component of the pyruvate-dehydrogenase complex;

xx) the aceF gene coding for the E2 component of the pyruvate-dehydrogenase complex;

yy) the pepB gene coding for aminopeptidase B;

zz) the aldH gene coding for aldehyde dehydrogenase,

aaa) the bfr gene coding for the iron-storage homoprotein;

bbb) the udp gene coding for uridine phosphorylase; and

ccc) the rseB gene coding for the regulator of sigmaE-factor activity.

13. The process of claim 1, wherein at least one metabolic pathway that diminishes the formation of said L-amino acid in said microorganism is at least partially eliminated.

14. The process of claim 1, wherein, said microorganism overexpressed said yfiD ORF and/or said pflB gene, and, in addition, the activity of the product of one or more additional genes is attenuated or eliminated or the expression of one or more additional genes or ORFs is diminished, said one or more additional genes being selected from the group consisting of:

a) the tdh gene coding for threonine dehydrogenase;

b) the mdh gene coding for malate dehydrogenase;

c) the open reading frame (ORF) yjfA;

d) the open reading frame (ORF) ytfP;

e) the pckA gene coding for phosphoenolpyruvate carboxykinase;

f) the poxB gene coding for pyruvate oxidase;

g) the aceA gene coding for isocitrate lyase;

h) the dgsA gene coding for the DgsA regulator of the phosphotransferase system;

i) the fruR gene coding for the fructose repressor;

j) the rpoS gene coding for the sigma38 factor;

k) the aspA gene coding for aspartate ammonium lyase; and

l) the aceB gene coding for malate synthase A.

15. The process of any one of claims 1-14, wherein said L-amino acid is selected from the group consisting of: L-asparagine, L-serine, L-glutamate, L-glycine, L-alanine, L-cysteine, L-valine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, L-histidine, L-lysine, L-tryptophan and L-arginine.

16. The process of any one of claims 1-14, wherein said L-amino acid is selected from the group consisting of: L-isoleucine, L-valine, L-methionine, L-homoserine and L-lysine are produced.

17. The process of any one of claims 1-14, wherein said L-amino acid is L-threonine.

18. A microorganism of the Enterobacteriaceae family in which the activity of the product of the yfiD ORF and/or the pflB gene is enhanced.

19. A microorganism of the Enterobacteriaceae family in which the yfiD ORF and/or the pflB gene is overexpressed or said microorganism has been transformed with a nucleotide sequence coding for the gene product of the yfiD ORF and/or the pflB gene.

20. The microorganism of either claim 18 or claim 19, wherein said microorganism is of the genus Escherichia.